In the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-26 (canceled)

27. (currently amended) A method of detecting a mismatch in any of a plurality of DNA duplexes of distinct nucleic acid sequence, said duplexes formed in a single hybridization reaction, comprising:

detecting, for any of said duplexes, an alteration in a bacterial cell characteristic, said alteration effected by the *in vivo* mismatch corepair of at least 5 contiguous nucleotides of a marker that is present together with said duplex in a vector within said bacterial cell, said corepair being initiated by a mismatch of no more than 4 contiguous nucleotides in said duplex.

28. (previously presented) The method of claim 27, wherein said plurality includes duplexes of at least 10 distinct nucleic acid sequences.

29. (previously presented) The method of claim 28, wherein said plurality includes at least 100 duplexes of distinct nucleic acid sequence.

30. (previously presented) The method of claim 29, wherein said plurality includes at least 10,000 duplexes of distinct nucleic acid sequence.

31. (previously presented) The method of claim 29, wherein said plurality includes at least 100,000 duplexes of distinct nucleic acid sequence.

32. (previously presented) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a prokaryote.

33. (previously presented) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a virus.

34. (previously presented) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a eukaryote.

35. (previously presented) The method of claim 34, wherein said eukaryote is a mammal.

36. (previously presented) The method of claim 35, wherein said mammal is a human.

37. (previously presented) The method of claim 36, wherein said plurality includes nucleic acid sequences derived from the coding region of a human gene.

38. (previously presented) The method of claim 37, wherein said human gene is selected from the group consisting of: hemoglobin, dystrophin, BRCA1, BRCA2, CFTR, factor VIII, factor IX, oncogenes, tumor suppressors, and genes on human chromosome 21.

39. (previously presented) The method of claim 27, wherein said mismatch in said duplex is a single nucleotide polymorphism.

40. (previously presented) The method of claim 27, wherein said marker is inactivated by said *in vivo* mismatch corepair.

41. (previously presented) The method of claim 27, wherein said marker is a recombinase.

42. (previously presented) The method of claim 41, wherein said recombinase is Cre recombinase.

43. (previously presented) The method of claim 27, wherein said bacterial cell characteristic is selected from the group consisting of: cell color, luminescence, antibiotic sensitivity, and antibiotic resistance.

44. (previously presented) The method of claim 41, wherein mismatch corepair of said recombinase alters said bacterial cell's antibiotic resistance or sensitivity.

45. (previously presented) The method of claim 27, further comprising the antecedent step of forming said plurality of DNA duplexes by annealing first nucleic acid strands, said first strands including at least one nucleic acid sequence, to second nucleic acid strands, said second strands including a plurality of distinct nucleic acid sequences.

46. (previously presented) The method of claim 45, wherein said plurality of second nucleic

acid strands are derived from a common source.

47. (previously presented) The method of claim 46, wherein said common source is genomic DNA from a single individual.

48. (previously presented) The method of claim 46, wherein said common source is cDNA from a single individual.

49. (previously presented) The method of claim 45, wherein said plurality of second nucleic acid strands are derived from a pooled source.

50. (previously presented) The method of claim 49, wherein said source is pooled from family members.

51-52. (canceled)